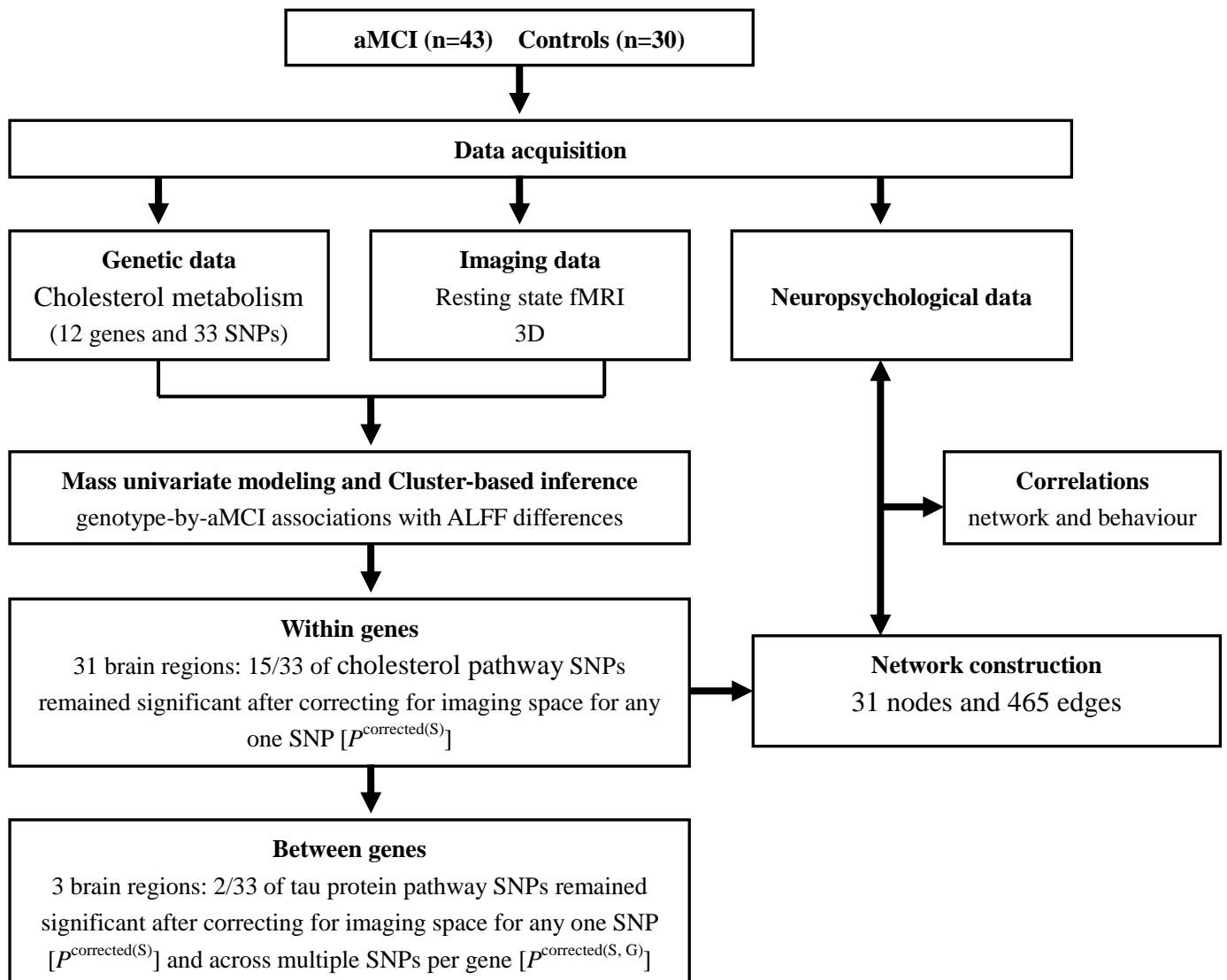


Multiple genetic imaging study of the association between cholesterol metabolism and brain functional alterations in individuals with risk factors for Alzheimer's disease

Supplementary Material

Part I. Overview of data process



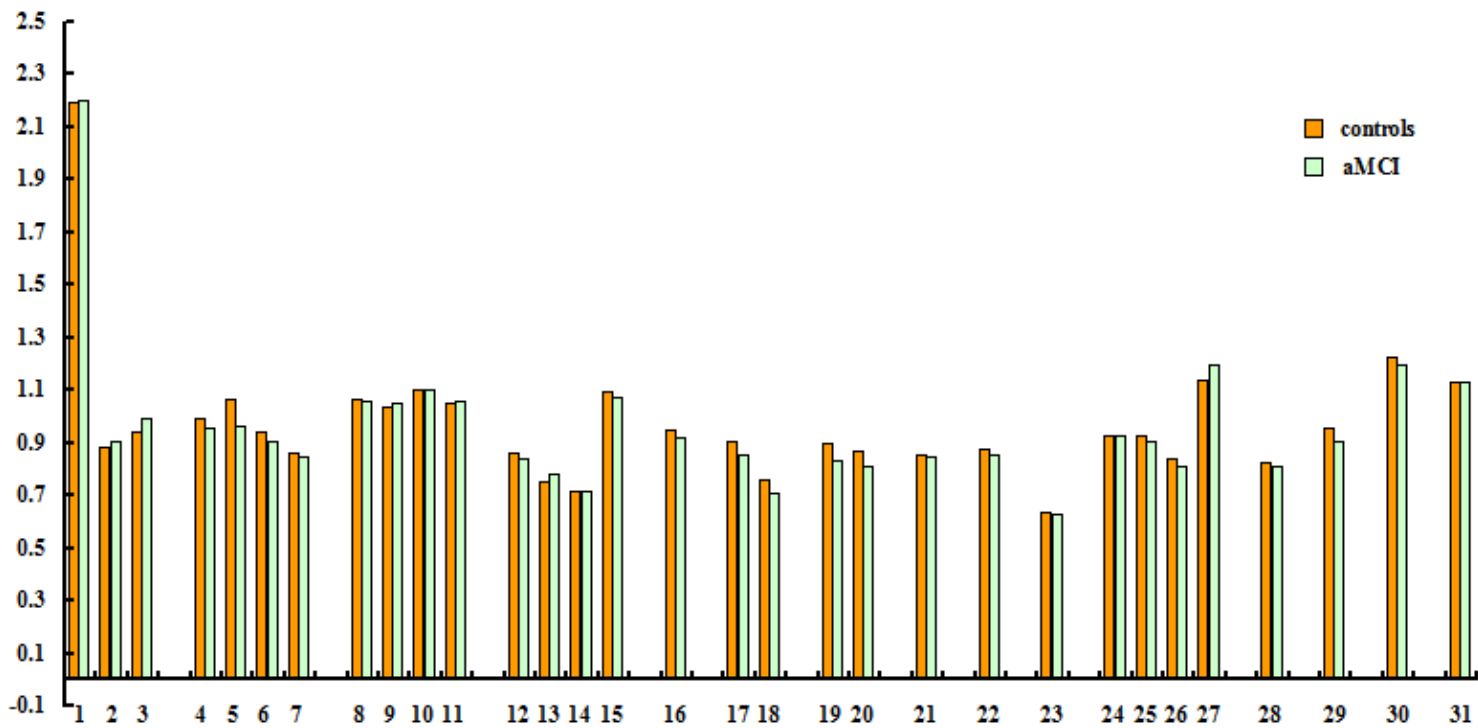
Part II. The details of mean ALFF values in all 31 regions of the 'SNP-by-status' interactions for the cholesterol metabolism pathway after correcting for imaging space for any one SNP ($P^{\text{corrected(S)}} < 0.05$), respectively.

ALFF values in all 31 regions of the 'SNP-by-status' interactions

Number	SNPs	Region	ALFF values		<i>P</i>
			Controls	aMCI	
ABCA1					
1	rs2230806	L.MOG	2.19±0.47	2.20±0.41	0.413
2		L.MFG	0.88±0.09	0.91±0.10	0.324
3		Vermis45	0.94±0.18	0.99±0.33	0.552
APOE					
4	rs7412	L.IFG	0.99±0.12	0.95±0.09	0.178
5		L.MTG	1.06±0.14	0.96±0.15	0.004*
6		R.INS	0.94±0.09	0.91±0.09	0.145
7		R. MCG	0.86±0.07	0.85±0.08	0.473
8	rs429358	L.CRBL_Po	1.07±0.25	1.06±0.20	0.598
9		R.STG	1.04±0.33	1.05±0.24	0.382
10		L.ACG	1.10±0.22	1.10±0.16	0.523
11		L.PHG	1.05±0.16	1.06±0.12	0.614
12	rs440446	R.PCUN	0.86±0.09	0.84±0.07	0.193
13		L.CRBL_Ant	0.75±0.09	0.78±0.12	0.239
14		R. CRBL_Po	0.72±0.08	0.72±0.09	0.955
15		L.MTG	1.10±0.15	1.07±0.18	0.388
CH25H					
16	rs4417181	R.MFG	0.95±0.09	0.92±0.08	0.433
CYP1					
17	rs754203	R.IFG	0.90±0.17	0.85±0.12	0.193
18		R.PHG	0.76±0.13	0.71±0.08	0.050*
19	rs7157609	R.IFG	0.90±0.17	0.83±0.13	0.088
20		R.PHG	0.87±0.13	0.81±0.10	0.045*
LDLR					
21	rs1433099	R.MeFG	0.85±0.13	0.85±0.12	0.805
22	rs2738444	R.IPL	0.87±0.13	0.85±0.07	0.964

LRP1					
23	rs1799986	R.ITG	0.63±0.11	0.63±0.10	0.920
LRP8					
24	rs5177	R.MFG	0.93±0.08	0.93±0.10	0.911
25		R.INS	0.92±0.08	0.93±0.10	0.480
26		R.PreCG	0.84±0.07	0.81±0.07	0.137
27		B.MeFG	1.14±0.20	1.20±0.26	0.902
28	rs3737983	R.SFG	0.82±0.14	0.81±0.12	0.991
29	rs3820198	L.Put	0.95±0.11	0.90±0.09	0.040*
MTHFR					
30	rs1801133	L.MOG	1.23±0.33	1.20±0.39	0.358
SOAT1					
31	rs3753526	L.IFG	1.13±0.15	1.13±0.20	0.695

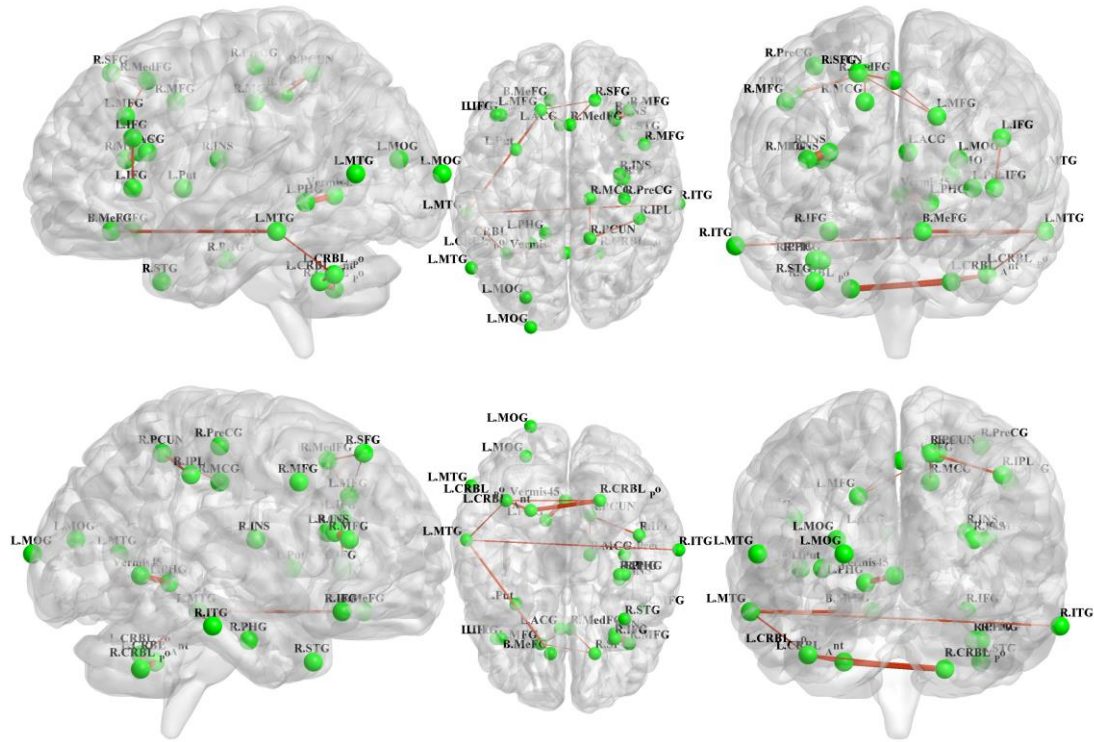
Values are the mean ± (SD); Notes: *P* value was obtained by the Mann-Whitney U-test. * indicates significant differences between groups, *P* < 0.05.



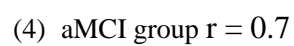
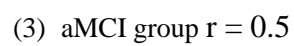
Part III. All 31 regions of genotype-by-aMCI interactions for cholesterol metabolism pathway after correcting for imaging space for any one SNP ($P^{\text{corrected}(S)} < 0.05$), which were marked out a unidirectional weighted network with 31 nodes and

465 edges that globally described the network connectivity patterns. The followings are the patterns of $r = 0.5$ and $r = 0.7$ in controls and aMCI, respectively.

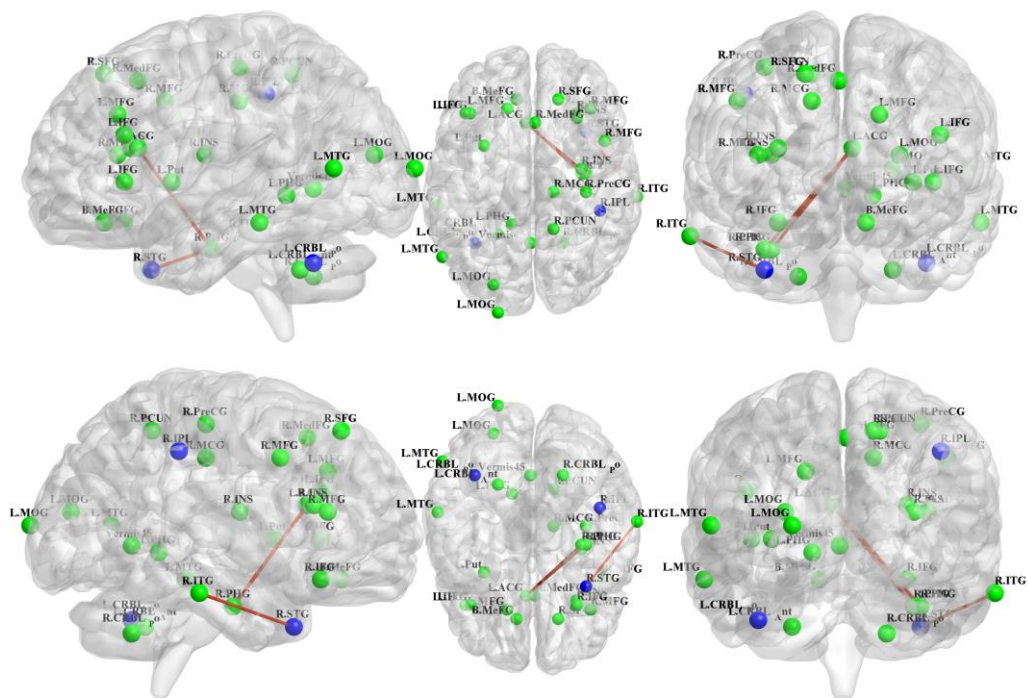
(1) Controls group $r = 0.5$



(2) Controls group $r = 0.7$



(2) $P < 0.01$



(3) $P < 0.001$

